



Title: Isoforms of the Human Vitamin D Receptor  
Inventor: Crofts et al.  
Application No.: 09/509,482  
Docket No.: RICE-014

FIG.1A

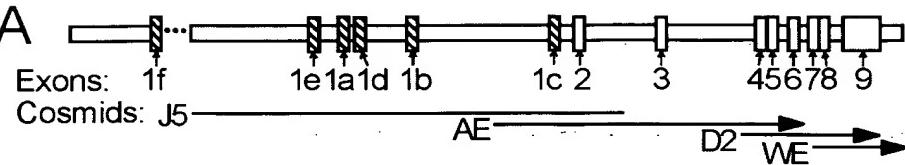
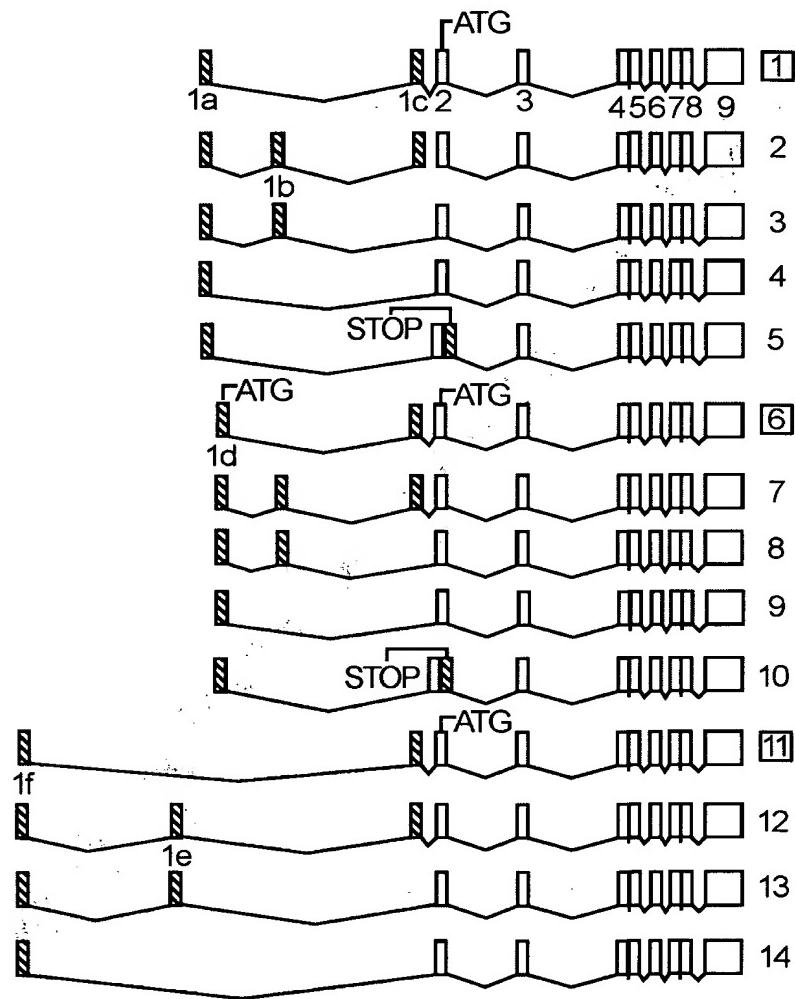


FIG.1B





## FIG. 1C

(SEQ ID NO.14) \_\_\_\_\_

Transcript 1:

Transcript 6:

Transcript 9:

MEAMA ASTSL PDPGD FDRNV PRI [DBD] 427aa  
MEAMA ASTSL PDPGD FDRNV PRI [DBD] 477aa  
MEW RNKKR SDWLS MVLRTAGVEG MEAMA ASTSL PDPGD FDRNV PRI [DBD] 450aa

(SEQ ID NO.16) \_\_\_\_\_

(SEQ ID NO.15) \_\_\_\_\_



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## FIG. 4

- A. 5'...atcccttaag GGCTOCTGAACTAGCCAGCTGGACGGAG  
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCC  
CGTGCACATTGCTTGCTGCCTCCCTCAATCCTCATAGCT  
TCTCTTGGAgttaagtacag...3' (SEQ ID NO: 13)
  
- B. 5'...TGCACCTGGCGGTGAGCCTGGGACAGGGGTGAGGC  
CAGAGACGGACGGACGCAGGGGCCGGCAGAAGGCGAGGG  
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG  
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC  
GCTGGTAGAAAGTTCTCCGAGGAGCCTGCCATCCAGTCGT  
GCGTGCAG...3' (SEQ ID NO: 5)
  
- C. 5'...tgttttttag AGGCAGCATGAAACAGTGGATGTGCAGAG  
AGAACGATCTGGGTCCAGTAGCTCTGACACTOCTCAGCTGT  
AGAAACCTTGACAACCTGACATCAGTTGTACAATGGAA  
CGGTATTTTACTCTCATGTCTGAAAAGGCTATGATAA  
AGATCAAAGtaagatatt...3' (SEQ ID NO: 6)
  
- D. 5'...GTTTCCTTCTTCTGTCGGGGCGCCTGGC**ATG**GAGTGG  
**AGGAATAAGAAAAGGAGCGATTGGCTGTCG**ATG**GTGCTCA**  
**GAAC TGCTGGAGTGGAGGgtgttaacc...3'** (SEQ ID NO: 1)



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FIG. 5A

## Transcript 6

(Sequence Range: 1 to 1463)

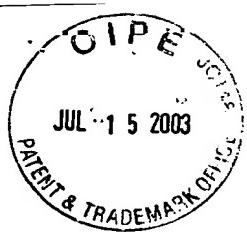


## FIG. 5B

410	420	430	440	450
*	*	*	*	*
CCACTGCCAG GCCTGCCGGC TCAAAACGCTG TGTGGACATC GGCATGATGA				
GGTGACGGTC CGGACGGCCG AGTTTGCAC ACACCTGTAG CCGTACTACT				
HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>				
460	470	480	490	500
*	*	*	*	*
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC				
TCCTCAAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG				
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>				
510	520	530	540	550
*	*	*	*	*
CTGAAGCGGA AGGAGGAGGA GGCTTGAAG GACAGTCTGC GGCCCAAGCT				
GACTTCGCCT TCCTCCTCCT CCGGAACCTTC CTGTCAGACG CCGGGTTCGA				
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>				
560	570	580	590	600
*	*	*	*	*
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA				
CAGACTCCTC' GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT				
SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>				
610	620	630	640	650
*	*	*	*	*
AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT				
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAACGGC CGGAGGTCAA				
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>				
660	670	680	690	700
*	*	*	*	*
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCA ACTCCAGACA				
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT				
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>				
710	720	730	740	750
*	*	*	*	*
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA				
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT				
ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>				
760	770	780	790	800
*	*	*	*	*
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG				
AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC				
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>				
810	820	830	840	850
*	*	*	*	*
AGTGAAGAAG ATTCAAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT				
TCACCTCTTC TAAGTCTACT GGGAGACAC TGGGATCTCG ACAGGGTCGA				
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>				

## FIG. 5C

860            870            880            890            900  
\*            \*            \*            \*            \*  
CTCCATGCTG CCCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG  
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTCC  
SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>  
  
910            920            930            940            950  
\*            \*            \*            \*            \*  
TCATTGGCTT TGCTAACGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG  
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC  
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>  
  
960            970            980            990            1000  
\*            \*            \*            \*            \*  
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG  
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC  
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>  
  
1010            1020            1030            1040            1050  
\*            \*            \*            \*            \*  
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC  
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG  
SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>  
  
1060            1070            1080            1090            1100  
\*            \*            \*            \*            \*  
AAGACTACAA GTACCCGGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG  
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTCGGCC TGTGTCGGAC  
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>  
  
1110            1120            1130            1140            1150  
\*            \*            \*            \*            \*  
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA  
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCTGACT TCTTCGACTT  
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>  
  
1160            1170            1180            1190            1200  
\*            \*            \*            \*            \*  
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC  
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG  
LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>  
  
1210            1220            1230            1240            1250  
\*            \*            \*            \*            \*  
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC  
GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG  
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>  
  
1260            1270            1280            1290            1300  
\*            \*            \*            \*            \*  
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCC  
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGG  
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>

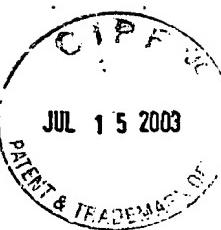


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## FIG. 5D

1310            1320            1330            1340            1350  
\*            \*            \*            \*            \*            \*            \*  
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC  
CCCGTCGGTG GACGAGATACTA GGTCTTACTA GGTCTTCGAT CGGCTGGACG  
GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>  
  
1360            1370            1380            1390            1400  
\*            \*            \*            \*            \*            \*            \*  
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG  
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC  
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>  
  
1410            1420            1430            1440            1450  
\*            \*            \*            \*            \*            \*            \*  
CCTGAGTGCA GCATGAAGCT AACGCCCTT GTGCTCGAAC TGTTTGGCAA  
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAAACCGTT  
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>  
  
1460  
\*            \*  
TGAGATCTCC TGA (SEQ ID NO:2)  
ACTCTAGAGG ACT (SEQ ID NO:17)  
GluIleSer \*\*\*>(SEQ ID NO:9)

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## FIG. 6A

Transcript 9

(Sequence range: 1 to 1382)

10            20            30            40            50  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
GTTTCCTTCT TCTGTGGGG CGCCTGGCA TGGAGTGGAG GAATAAGAAA  
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT  
MetGluTrpArg AsnLysLys>  
  
60            70            80            90            100  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT  
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCTA  
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>  
  
110            120            130            140            150  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
GGAGGCAATG GCGGCCAGCA CTTCCTGCC TGACCCCTGGA GACTTGACC  
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG  
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>  
  
160            170            180            190            200  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
GGAACGTGCC CGGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT  
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA  
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>  
  
210            220            230            240            250  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG  
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC  
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>  
  
260            270            280            290            300  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
CATGAAGCGG AAGGCACTAT TCACCTGCC CTTCAACGGG GACTGCCGCA  
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCC CTGACGGCGT  
MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>  
  
310            320            330            340            350  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT  
AGTGGTTCT GTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA  
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>  
  
360            370            380            390            400  
\* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \* \*  
GTGGACATCG GCATGATGAA GGAGTTCAATT CTGACAGATG AGGAAGTGCA  
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT  
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>

## FIG. 6B

410            420            430            440            450  
\*            \*            \*            \*            \*            \*  
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGGAGG GCCTTGAGG  
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACCTCC  
ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

460            470            480            490            500  
\*            \*            \*            \*            \*            \*  
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCACGCGCAT CATTGCCATA  
TGTCAAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT  
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

510            520            530            540            550  
\*            \*            \*            \*            \*            \*  
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG  
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC  
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

560            570            580            590            600  
\*            \*            \*            \*            \*            \*  
CCAGTTCCCG CCTCCAGTTC GTGTGAATGA TGTTGGAGGG AGCCATCCTT  
GGTCAAGGCC GGAGGTCAG CACACTTACT ACCACCTCCC TCGGTAGGAA  
GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

610            620            630            640            650  
\*            \*            \*            \*            \*            \*  
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGA CTCCTCCTCC  
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG  
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

660            670            680            690            700  
\*            \*            \*            \*            \*            \*  
TCCTGCTCAG ATCACTGTAT CACCTTTCA GACATGATGG ACTCGTCCAG  
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC  
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

710            720            730            740            750  
\*            \*            \*            \*            \*            \*  
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAAGATGAC CCTTCTGTGA  
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT  
PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

760            770            780            790            800  
\*            \*            \*            \*            \*            \*  
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC  
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAAG  
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

810            820            830            840            850  
\*            \*            \*            \*            \*            \*  
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAAGATGA TACCAGGATT  
TCAATGTCGT AGGTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA  
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>

## FIG. 6C

860            870            880            890            900  
\* \* \* \* \*  
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA  
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT  
ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>  
  
910            920            930            940            950  
\* \* \* \* \*  
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAC GGACGACATG  
AACTCCAGTA GTACAAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC  
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>  
  
960            970            980            990            1000  
\* \* \* \* \*  
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACCGTGAC  
AGGACCTGGA CACCGTTGGT TCTGATGTTA ATGGCGCAGT CACTGCACTG  
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>  
  
1010           1020           1030           1040           1050  
\* \* \* \* \*  
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG  
GTTTCGGCCT GTGTGGACCC TCGACTAACT CGGGGAGTAG TTCAAGGTCC  
LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>  
  
1060           1070           1080           1090           1100  
\* \* \* \* \*  
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG  
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC  
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>  
  
1110           1120           1130           1140           1150  
\* \* \* \* \*  
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT  
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA  
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>  
  
1160           1170           1180           1190           1200  
\* \* \* \* \*  
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC  
CTAACTCCGG TAGGTCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG  
IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>  
  
1210           1220           1230           1240           1250  
\* \* \* \* \*  
GCTGCCGCCA CCCGCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC  
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG  
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>  
  
1260           1270           1280           1290           1300  
\* \* \* \* \*  
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA  
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT  
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>

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## FIG. 6D

1310            1320            1330            1340            1350  
\*       \*       \*       \*       \*       \*       \*       \*       \*  
CCGCTGCCTC TCCTTCCAGC CTGAGTCAG CATGAAGCTA ACGCCCCTTG  
GGCGACGGAG AGGAAGGTG GACTCACGTC GTACTTCGAT TGCGGGAAAC  
ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>  
  
1360            1370            1380  
\*       \*       \*       \*       \*       \*  
TGCTCGAACGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3)  
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18)  
ValLeuGluVal PheGlyAsn GluIleSer \*\*\*> (SEQ ID NO:10)

## FIG. 7A

Transcript 10  
(Sequence Range: 1 to 1534)

10            20            30            40            50  
\* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*  
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGAGTGGAG GAATAAGAAA  
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT  
MetGluTrpArg AsnLysLys>  
  
60            70            80            90            100  
\* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*  
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT  
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA  
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>  
  
110            120            130            140            150  
\* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*  
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCCTGGA GACTTTGACC  
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG  
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>  
  
160            170            180            190            200  
\* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*  
GGAACGTGCC CGGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT  
CCTTGCACGG GGCTTAGACA CCCCCACACAC CTCTGGCTCG GTGACCGAAA  
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>  
  
210            220            230            240            250  
\* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*  
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC  
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG  
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg\*\*\* (SEQ ID NO:11)  
  
260            270            280            290            300  
\* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*  
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG  
GGGGGAGGGT CCGAGAGGGG TCACCTTTCCT CTCCTCTTC TTCGTTCCAC  
  
310            320            330            340            350  
\* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*  
TTTCCATGAA GGGAGCCCTT GCATTTTCA CATCTCCCTTC CTTACAATGT  
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA  
  
360            370            380            390            400  
\* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*      \* \* \* \* \*CCATGGAACA TGGGGCGCTC ACAGGCCACAG GAGCAGGAGG GTCTTGGCGA  
GGTACCTTGT ACGCCGCGAG TGTCGGTGTG CTCGTCCTCC CAGAACCGCT



## FIG. 7B

410            420            430            440            450  
\* \*            \* \*            \* \*            \* \*            \* \*  
AGCATGAAGC GGAAGGC ACT ATT CAC CTG C CCCT CAAC G GGGACTGCC G  
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAAGTTGC CCCTGACGGC  
  
460            470            480            490            500  
\* \*            \* \*            \* \*            \* \*            \* \*  
CATCACCAAG GACAACC GAC GCC ACTGCCA GGCCTGCCGG CTCAAACGCT  
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA  
  
510            520            530            540            550  
\* \*            \* \*            \* \*            \* \*            \* \*  
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG  
CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC  
  
560            570            580            590            600  
\* \*            \* \*            \* \*            \* \*            \* \*  
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA  
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCCTCCTCC TCCGGAACCT  
  
610            620            630            640            650  
\* \*            \* \*            \* \*            \* \*            \* \*  
GGACAGTCTG CGGCCAACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC  
CCTGTCAGAC GCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT  
  
660            670            680            690            700  
\* \*            \* \*            \* \*            \* \*            \* \*  
TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC  
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG  
  
710            720            730            740            750  
\* \*            \* \*            \* \*            \* \*            \* \*  
TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC  
ACGGTCAAGG CGGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG  
  
760            770            780            790            800  
\* \*            \* \*            \* \*            \* \*            \* \*  
TTCCAGGCC C AACTCCAGAC ACACCTCCAG CTTCTCTGGG GACTCCTCCT  
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA  
  
810            820            830            840            850  
\* \*            \* \*            \* \*            \* \*            \* \*  
CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC  
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG  
  
860            870            880            890            900  
\* \*            \* \*            \* \*            \* \*            \* \*  
AGCTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAAGATG ACCCTCTGT  
TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA  
  
910            920            930            940            950  
\* \*            \* \*            \* \*            \* \*            \* \*  
GACCCTAGAG CTGTCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG  
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC

FIG. 7C

960            970            980            990            1000  
\*            \*            \*            \*            \*            \*  
TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA  
AGTCAATGTC GTAGGTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT  
  
1010            1020            1030            1040            1050  
\*            \*            \*            \*            \*            \*  
TTCAGAGACC TCACCTCTGA GGACCAAGATC GTACTGCTGA AGTCAAGTGC  
AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG  
  
1060            1070            1080            1090            1100  
\*            \*            \*            \*            \*            \*  
CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA  
GTAACCTCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT  
  
1110            1120            1130            1140            1150  
\*            \*            \*            \*            \*            \*  
TGTCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG  
ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC  
  
1160            1170            1180            1190            1200  
\*            \*            \*            \*            \*            \*  
ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCCTCA TCAAGTTCCA  
TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT  
  
1210            1220            1230            1240            1250  
\*            \*            \*            \*            \*            \*  
GGTGGGACTG AAGAACGCTGA ACTTGATGAA GGAGGAGCAT GTCCTGCTCA  
CCACCCCTGAC TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT  
  
1260            1270            1280            1290            1300  
\*            \*            \*            \*            \*            \*  
TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG  
ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCCG  
  
1310            1320            1330            1340            1350  
\*            \*            \*            \*            \*            \*  
CTGATTGAGG CCATCCAGGA CCCCTGTCC AACACACTGC AGACGTACAT  
GACTAACTCC GGTAGGTCTT GGCGGACAGG TTGTGTGACG TCTGCATGTA  
  
1360            1370            1380            1390            1400  
\*            \*            \*            \*            \*            \*  
CCGCTGCCGC CACCCGCCCG CGGGCAGCCA CCTGCTCTAT GCCAAGATGA  
GGCGACGGCG GTGGGGGGGG GCCCCTCGGT GGACGAGATA CGGTTCTACT  
  
1410            1420            1430            1440            1450  
\*            \*            \*            \*            \*            \*  
TCCAGAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG  
AGGTCTTCGA TCGGCTGGAC CGTCGGAGT TACTCCTCGT GAGGTTCGTC  
  
1460            1470            1480            1490            1500  
\*            \*            \*            \*            \*            \*  
TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCT  
ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA

O P E  
JUL 15 2003  
PATENT & TRADEMARK OFFICE  
Title: Isoforms of the Human Vitamin D Recep  
Inventor: Crofts et al.  
Application No.: 09/509,482  
Docket No.: RICE-014

## FIG. 7D

1510

1520

1530

\* \* \* \* \*

TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)  
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)

## FIG. 8A

10            20            30            40            50  
\*            \*            \*            \*            \*  
TGC GAC CTT GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG  
ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC

60            70            80            90            100  
\*            \*            \*            \*            \*  
GACGCAGGGGG CCCGGCCCAA GGCAGGGGAG AACAGCAGCA CTAAGGCAGA  
CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT

110            120            130            140            150  
\*            \*            \*            \*            \*  
AAGGAAGAGGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC  
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG

160            170            180            190            200  
\*            \*            \*            \*            \*  
TCCTAGACGC TGGTAGAAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG  
AGGATCTGCG ACCATTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC

210            220            230            240            250  
\*            \*            \*            \*            \*  
CGTGCAGAACG CCTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAACAGC  
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG

260            270            280            290            300  
\*            \*            \*            \*            \*  
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCCA  
TGGGGACCCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT  
MetGluAla>

310            320            330            340            350  
\*            \*            \*            \*            \*  
TGCGGGCCAG CACTTCCCTG CCTGACCCCTG GAGACTTTGA CCGGAACGTG  
ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTGCAC  
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>

360            370            380            390            400  
\*            \*            \*            \*            \*  
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA  
GGGGCCTAGA CACCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT  
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>

410            420            430            440            450  
\*            \*            \*            \*            \*  
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAGGCAGA AGCATGAAGC  
ACGATACTGG ACACTTCCGA CGTTCCGAA GAAGTCCGCT TCGTACTTCG  
AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>

460            470            480            490            500  
\*            \*            \*            \*            \*  
GGAAGGCACT ATTACACCTGC CCCTTCAACG GGGACTGCCG CATCACCAAG  
CCTTCCGTGA TAAGTGGACG GGGAAAGTTGC CCCTGACGGC GTAGTGGTTC  
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>



Title: Isoforms of the Human Vitamin D Receptor  
 Inventor: Crofts et al.  
 Application No.: 09/509,482  
 Docket No.: RICE-014

## FIG. 8B

510	520	530	540	550
*	*	*	*	*
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTGCGA CACACCTGTA AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>				
560	570	580	590	600
*	*	*	*	*
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC GCCGTACTAC TTCCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>				
610	620	630	640	650
*	*	*	*	*
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG CCCCTCTACTA GGACTTCGCC TTCCCTCTCC TCCGGAACCT CCTGTCAGAC ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>				
660	670	680	690	700
*	*	*	*	*
CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>				
710	720	730	740	750
*	*	*	*	*
CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC CGGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>				
760	770	780	790	800
*	*	*	*	*
GCCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCC CCGGAGGTCA AGCACACTA CTACCACCTC CCTCGGGTAGG AAGGTCCGGG ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>				
810	820	830	840	850
*	*	*	*	*
AACTCCAGAC ACACCTCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>				
860	870	880	890	900
*	*	*	*	*
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>				
910	920	930	940	950
*	*	*	*	*
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG TAGACCTAGA CTCACCTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>				
960	970	980	990	1000
*	*	*	*	*
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG GACAGGGTCTG AGAGGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>				

## FIG. 8C

1010        1020        1030        1040        1050  
\*            \*            \*            \*            \*  
CATCCAAAAG GTCATTGGCT TTGCTAACAGT GATACCAGGA TTCAGAGACC  
GTAGGTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG  
IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>  
  
1060        1070        1080        1090        1100  
\*            \*            \*            \*            \*  
TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC  
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG  
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>  
  
1110        1120        1130        1140        1150  
\*            \*            \*            \*            \*  
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCCTGGAC  
TAGTACAAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG  
IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>  
  
1160        1170        1180        1190        1200  
\*            \*            \*            \*            \*  
CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG  
GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC  
CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>  
  
1210        1220        1230        1240        1250  
\*            \*            \*            \*            \*  
GACACAGCCT GGAGCTGATT GAGCCCCCTCA TCAAGTTCCA GGTGGGACTG  
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCCTGAC  
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>  
  
1260        1270        1280        1290        1300  
\*            \*            \*            \*            \*  
AAGAAAGCTGA ACTTGCATGA GGAGGGAGCAT GTCCCTGCTCA TGGCCATCTG  
TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC  
LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>  
  
1310        1320        1330        1340        1350  
\*            \*            \*            \*            \*  
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG  
GTAGCAGAGG GGTCTAGCAG GACCCCCACGT CCTGCGGCGC GACTAACTCC  
IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>  
  
1360        1370        1380        1390        1400  
\*            \*            \*            \*            \*  
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC  
GGTAGGTCTT GGCAGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG  
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>  
  
1410        1420        1430        1440        1450  
\*            \*            \*            \*            \*  
CACCCGCCCG CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT  
GTGGGGCGGGG GCCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA  
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>  
  
1460        1470        1480        1490        1500  
\*            \*            \*            \*            \*  
AGCCGACCTG CGCAGCCTCA ATGAGGGAGCA CTCCAAGCAG TACCGCTGCC  
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG  
AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>

## FIG. 8D

1510            1520            1530            1540            1550  
\*                \*                \*                \*                \*  
TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCT TGTGCTCGAA  
AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT  
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>  
  
1560            1570  
\*                \*  
GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:7)  
CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:20)  
ValPheGly AsnGluIleSer \*\*\*> (SEQ ID NO:12)